IN THE SPECIFICATION

Please amend the specification as follows:

The paragraph beginning at page 6, line 4 is amended as follows:

For the identification of unknown organisms, the entire (mostly 16S) rDNA, as a rule, is amplified with two universal primers per PCR, and s subsequently sequenced. In this way, extensive rDNA databases have developed containing at present sequences of several thousands of organisms (e.g. RDP/Ribosomal Database Project II, Michigan State University, ~~http://www.cme.msu.edu/RDP~~) allowing the phytogenetic assignment of new sequences. This method, in principle, allows the detection of any arbitrary organism, but is very time-consuming and therefore inappropriate for diagnostic applications. Moreover, the process is affected by a series of error sources (F. Wintzingerrode, U.B. Goebel, E. Stackebrand; Determination of microbial diversity in environmental samples: pitfalls of PCR-based rRNA analysis. FEMS Microbiology Reviews, 1997, 21:213-229), whereby, in particular, recombination processes and point mutation lead to false results during the PCR amplification.

Please add the following heading at page 10, line 6 as follows:

Brief Description of the Drawings